

Scoring table:	Scoring table: IDENTITY NUC Gapov 10.0 , Gapext 1.0	Post-processing: Minimum DB seq length: 0 Maximum DB seq length: 20000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	RESULT 1
Title:	US-10-814-858A-2			CG206846 /C
Perfect score:	130			LOCUS CG206846
Sequence:	1 tcactatatacgaaagtcc.....ttacatctgatataacaatgt 130			DEFINITION TOS047 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza sativa (japonica cultivar-group) genomic clone TOSJNBNh019II10h,
Scoring table:	Scoring table: IDENTITY NUC Gapov 10.0 , Gapext 1.0			ACCESSION CG206846
Searched:	34239544 seqs, 19032134700 residues			VERSION CG206846.1 GI:34097907
Total number of hits satisfying chosen parameters:	68479088			KEYWORDS GSS
Minimum DB seq length:	0			SOURCE Oryza sativa (japonica cultivar-group)
Maximum DB seq length:	20000000000			ORGANISM Oryza sativa (japonica cultivar-group)
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries				Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
Database :	EST: * 1: gb_est1: * 2: gb_est2: * 3: gb_htc: * 4: gb_est3: * 5: gb_est4: * 6: gb_est5: * 7: gb_est6: * 8: gb_ssb1: * 9: gb_gss2: *			Ehrhartoideae; Oryzeae; Oryzae.
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	1 (bases 1 to 54)			AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.
SUMMARIES				TITLE BAC end sequences to close the gaps of a rice physical map at TAMU Unpublished (2003)
Result No.	Score	Query Match	Length DB	ID . Description
C 1	48	36.9	654	CG206846 TOS046 T A2679757 ENT013TF
C 2	42.6	32.8	884	A2679757 ENT013TF
C 3	42.6	32.8	888	A2650547 ENT0270TF
C 4	42.6	32.8	935	AZ684425 ENT0589TR
C 5	39.8	30.6	424	BP617758 BP617758
C 6	39.8	30.6	1093	CR25951 Tetraodon
C 7	39	30.0	490	AZ045132 Gm UMb001
C 8	38.8	29.8	821	BH249781 BOGX07TF
C 9	38.8	29.8	963	CNS0EBZ0
C 10	38.2	29.4	523	AAB46861 AJ42611
C 11	37.8	29.1	530	AZ522110 202bbC04
C 12	37.9	29.1	979	AZ96694 Tetraodon
C 13	37.4	28.8	572	BJS89243 BJ495243
C 14	37.4	28.8	628	BJS89532 BJ39532
C 15	37.4	28.8	752	AV711184 AV711184
C 16	37.2	28.6	917	CG53396 MBEDD83TR
C 17	37	28.5	1067	AL322699 Tetraodon
C 18	36.6	28.2	502	BJ440260 icTf03
C 19	36.6	28.2	893	AZ534920 ENTG21TR
C 20	36.6	28.2	898	AZ693862 ENTR46TR
C 21	36.6	28.2	1198	CR697279 Tetraodon
C 22	36.6	28.2	1273	CL49111 CH213-131
C 23	36.4	28.0	513	AZ233942 RPC1-23-7
C 24	36.4	28.0	2689	AG390466 Mus muscu

Query Match 36.9%; Score 48; DB 9; Length 654;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 63; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

45	TGTATTTCTAACATTACAAACAACAAACAAACAAACAAACATTACATTACTAT	104
156	TCTATTTTACAACTTACAAACAAACAAACAAACAAACAAACAT - TACAACTAT	99
105	TTACAAATTAC	114
98	TTACAAATTAC	89

RESULT 3  
AZ50547/c  
LOCUS  
DEFINITION

SECTION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 SULT 2  
 679757/C  
 CDS  
 DEFINITION A2679757 ENTamoeba histolytica linear GSS 14 - DEC-2000  
 ENTamoeba histolytica Sheared DNA Entamoeba histolytica  
 Genomic survey sequence.  
 SESSION A2679757

A2679757.1 GI:11816903  
 WORDS GSS.  
 SOURCE Entamoeba histolytica  
 ORGANISM Entamoeba histolytica  
 DIFFERENCE Entamoeba; Entamoebidae; Entamoeba.  
 AUTHORS Loftus B., Van Aken,S., and Fraser,C.  
 TITLE Determination of clone end sequences from Entamoeba histolytica  
 HML:IMSS sheared DNA library  
 DATE 2000-01-01  
 SOURCE 1

unpublished (2000)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel.: 301 838 0208  
Fax: 301 838 3543  
Email: [bjloftus@tigr.org](mailto:bjloftus@tigr.org)  
Clones are derived from the *Entamoeba histolytica* HM1:IMSS sheared DNA library

Seq primer: M13-Forward  
 Class: shotgun  
 High quality sequence start: 15  
 High quality sequence stop: 806.  
 Location/Qualifier:  
 1. .884  
 /organism="Entamoeba histolytica"  
 /mol\_type="Genomic DNA"  
 /strain="RM1:INSS"  
 /db\_xref="LcXon:5759"  
 /clone\_id="Entamoeba histolytica Sheared DNA"  
 /note="Vector: pHOSt; Site\_1: Bst I; Constructed at The  
 Institute for Genomic Research (TIGR), Rockville, MD;  
 Genomic DNA isolated from broth cultures of *E. histolytica*  
 using a method described by Clark and Diamond (Clark,  
 C.G., and Diamond, L.S. (1993) Entamoeba histolytica:  
 method for isolate identification. *Exp. Parasit.* 77:4450.) The DNA was mechanically sheared to give a  
 tight size distribution (< 1 kb).  
 source .

The library construction is described in detail in Smith, H.O., and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

RY Match	Score	DB	Length
Local Similarity	42.6	8	884
Matches	61.1%	Pred. No.	5.3
Conservative	69	Mismatches	0
		Indels	0
		Gaps	0
18	TTCATTCAATTGGAACTGAGCTGTGTCATTTCTCAACATTACAAACACACAAA	77	
551	TTCATTCAATTATCTCTTCAACTATCTTAATTACGAACTCTAATCCTAAACGTAA	492	
78	CACAAACACATTATAAACATTACTATTCAATTATCATCTGAGATAACATG	130	
491	CAACAAATTAAATTATTTAAAGGAAATAACAAAGATTGTAATTAAATTC	129	

**RESULT** 3  
 AZ50547/c  
**LOCUS** AZ50547  
**DEFINITION** ENTFZ70T Entamoeba histolytica  
**ACCESSION** GSS 14-NOV-2000  
 888 bp DNA linear Sheared DNA Entamoeba histolytica  
 Genomic, genomic survey sequence.  
 Accession number.

A255054 /	
VERSION	A2550547 .1
SOURCE	GI:11175848
ORGANISM	GSS .
REFERENCE	Entamoeba histolytica
AUTHORS	Entamoeba histolytica
	Eukaryota; Entamoebidae; Entamoeba .
	1 /bases 1 to 888
	Loftus,B., Van Aken,S. and Pradhan,C.

JOURNAL COMMENT  
determination of clone end sequences from *Entamoeba histolytica*  
HMI:IMSS sheared DNA library  
Unpublished (2000)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543

Email: [Djorlute@tigr.org](mailto:Djorlute@tigr.org)  
 Clones are derived from the *Brentamoeba histolytica* HM1:IMSS sheared  
 DNA library  
 Seq primer: M13-Forward  
 Class: shotgun  
 High quality sequence start: 16  
 High quality sequence stop: 863.  
 Location/Qualifiers  
 1..888  
 /organism="Entamoeba histolytica"  
 FEATURES  
 source

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/mot_type="genomic DNA"
/strain="THM1:IMSS"
/db xref="Taxon:5759"
/clone lib="Entamoeba histolytica"
/note="Vector: phOS1; Site 1: BST I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD
using a method described from broth cultures of E. histolytica
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol. 77:450.).
The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + method used for
the library construction is described in detail in Smith,
H.O. and Ventner, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999 "ORIGIN
```

VERSION AZ684425.1 GI:1118215  
KEYWORDS GSS.  
SOURCE Entamoeba histolytica

ORGANISM	Entamoeba histolytica Eukaryota; Entamoebidae; Entamoeba. 1 (bases 1 to 935)	TITLE	Functional annotation of a full-length Arabidopsis cDNA collection Science 296 (5565), 141-145 (2002) 2193900
REFERENCE	Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HM1:IMSS sheared DNA library	JOURNAL	PUBLISHED 11910074 COMMENT Contact: Motoaki Seki Plant Functional Genomics Research Group RIKEN Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-4359 Fax: 81-298-36-9060 Email: msski@rci.riken.go.jp reversed clone; Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for further details.
AUTHORS		FEATURES	source 1. -424 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db_xref="taxon:3702" /clone="RAFL16-25-F22" /lab_host="DH10B" /clone_1ib="RAFL16" /note="Site_1: BamHI; Site_2: SalI; dark-green" /Location/Qualifiers
TITLE		ORIGIN	
COMMENT	Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute For Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3543 Fax: 301 838 3543 Email: bjloftus@igc.org Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library	Query Match	Score 39.8; DB 5; Length 424; Best Local Similarity 59.1%; Pred. No. 27; Matches 68; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
UNPUBLISHED		Qy	15 AAGTCATTCTATTGGATGGACAGCTGTTGCAATTCAACAACTTCAACAAAC 74 34 ATCTTCATCATATAAGCTAAATCAGAGCTTCTTCAAGCATTCCATCGAAC 93
UNPUBLISHED (2000)		Db	75 AACACAAACACATTATACATACTATTACAAATTACATCTAGATAAACAT 129 94 AACAGTAACAAAAGTAAAGGTAAAAACACAACTACCGTAAAAAAGCAA 148
CONTACT		RESULT 6	CR/25951/c
BRENDAN J LOFTUS		LOCUS	CR725951 1093 bp mRNA linear HRC 19-AUG-2004
THE INSTITUTE FOR GENOMIC RESEARCH		DEFINITION	Tetraodon nigroviridis full-length cDNA.
9712 MEDICAL CENTER DR., ROCKVILLE, MD 20850		ACCESSION	CR725951
TEL: 301 838 3543		VERSION	GI:51242202
FAX: 301 838 3543		KEYWORDS	HTC; cDNA; Tetraodon nigroviridis
E-mail: bjloftus@igc.org		SOURCE	Tetraodon nigroviridis
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percromorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
		REFERENCE	1 (bases 1 to 1093)
		AUTHORS	Genoscope.
		TITLE	Direct Submission.
		JOURNAL	Submitted (10-AUG-2004) Genoscope - Centre National de Séquençage -
		COMMENT	: 2 rue Gaston Crèmeux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
		FEATURES	The sequences are based on single pass reads. More information available at http://www.genoscope.cns.fr/tetraodon.
		source	1. -1093 /organism="Tetraodon nigroviridis" /mol_type="mRNA" /tissue_type="fish"
		ORIGIN	
RESULTS 5		Query Match	Score 39.8; DB 3; Length 1093;
BP617758	BP617758 RAFL16 424 bp mRNA linear EST 26-JUN-2004	DEFINITION	Centre National de Séquençage -
DEFINITION	mRNA sequence.	VERSION	BP617758
VERSION	BP617758.1 GI:49268940	KEYWORDS	EST.
KEYWORDS	Arabidopsis thaliana (thale cress)	SOURCE	Arabidopsis thaliana
ORGANISM	Bukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	ORGANISM	Nakajima, M.; Marusaka, M.; Kamiya, A.; Ishida, J.; Satou, M.; Sakurai, T.; Nakajima, M.; Enju, A.; Akiyama, K.; Ono, Y.; Muramatsu, M.; Hayashizaki, Y.; Kawai, J.; Carninci, P.; Itoh, M.; Ishii, Y.; Arakawa, T.; Shibaoka, K.; Shinagawa, A. and Shinozaki, K.
REFERENCE	1 (bases 1 to 424)	LOCUS	BP617758 RAFL16 424 bp mRNA linear EST 26-JUN-2004
AUTHORS		DEFINITION	5 TATATATAGGAACCTCATTCATTGAAATGACACTGTTCTCACAAATTAC 64

Db	483	TATTAAGTGAATCATTGTTGTAGCAACTGAACTGAAAGTAAAC	4 24	Qy	5	TATATAAGGAGTCATTCAATTGGATGGCACGCTTGCATTCTCACAAATTAC	64
Qy	65	CAACACAACAAACAAACAAACATTAATTACATTACATTACATTACATTAC	124	Db	250	TATATAATGACATTCAATTGGTAGGCAACGTTGCTTCTCACAAATTAC	64
Db	423	CAAATATGAAACCACTAAAGATGCACTAAATGAAATTACAAATTAA	364	Qy	65	CAACACAACAAACAAACATTAATTACATTACATTACATTACATTACATTAC	309
Qy	125	ACA 127		Db	310	CTACCATATAGACGAAAAGATGAAATTACATTAATNNAAAATACARA	124
Db	363	AAA 361		Qy	125	ACAA 128	369
RESULT <sup>*</sup> 7				Db	370	ATAA 373	
LOCUS	AZ045132	490 bp	DNA	linear	GSS 31-JAN-2003		
DEFINITION	Gm_UMB001_025_G19P	UNN	Soybean BAC Library	(PECSBAC4 EcoRI)	Glycine		
max genomic clone	Glycine max	genomic	clone	Gm_UMB001_025_G19,			
GENOMIC SURVEY SEQUENCE	AZ045132	1	GR:7191282				
VERSION	GSS						
KEYWORDS	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.						
AUTHORS	Larson, K., Mudge, J., Cooper, A., Grivna, S., Denny, R., Penuela, S., Danesh, D. and Young, N.D.						
TITLE	BAC End sequences from a soybean genomic library (UMN)						
JOURNAL	Unpublished (1999)						
COMMENT	Contact: Young Nevin D Department of Plant Pathology University of Minnesota 495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA Tel: 612 625 2225 Fax: 612 625 9728 Email: nevin@tc.umn.edu						
REFERENCE	Sequence on contig Gm_A963_ctg_a near mapped duplicate of REFLP probe PA963 on Linkage Group F. For more information, see Soybase at: <a href="http://soybase.euron.iasante.edu">http://soybase.euron.iasante.edu</a> . Please see as an authority for the mapping/naming: Cregan, P.B., T. Jarvik, A.L. Bush, R.C. Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490						
FEATURES	Seq Primer: Mj3F Class: BAC ends						
Source	Location/Qualifiers	1..490					
	/organism="Glycine max"						
	/cultivar="Paribault"						
	/db_xref="taxon:3647"						
	/issue_type="coryledon_leaves"						
	/dev_stage="coryledon_leaves"						
	/clone_lib="UMN Soybean BAC Library (PECSBAC4 EcoRI)"						
	/note="Vector: PECSBAC4; The UMN BAC library (Danesh et al. Theor. Appl. Genet. 96:196, 1998) was constructed using the Eco RI site of PECSBAC4. The library consists of 72,960 clones with an average insert size of 120 Kb. Library is done by hybridization of high-density colony filters and/or PCR amplification of DNA pools. Four high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."						
ORIGIN	Query Match Score 30.0%; Best Local Similarity 55.6%; Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;	963 bp	DNA	linear	GSS 01-SEP-2002		
	RESULT 9						
	CNS03EZ0/c						
	LOCUS						

DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone sequence 021G13 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION AL241029

VERSION 1

KEYWORDS GSS; genome survey sequence.

SOURCE Tetraodon nigroviridis

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Percomorpha; Tetraodontiformes; Tetradontoidae; Tetradontidae; Tetradon.

REFERENCE Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fischer,C., Bernot,A., Pizames,C., Wincker,P., Brottier,P., Quétier,F., Saurin,W. and Weissenbach,J.

AUTHORS Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

TITLE Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL 20296633

MEDLINE 10835645

PUBMED 2

REFERENCE Roest Crollius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Pizames,C., Fischer,C., Bouneau,L., Billault,A., Quétier,F., Saurin,W., Bernot,A. and Weissenbach,J.

AUTHORS Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

JOURNAL Genome Res. 10 (7), 939-949 (2000)

MEDLINE 20359837

PUBMED 1089143

REFERENCE 3 (bases 1 to 963)

JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Séquençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES Source

1. 963 /organism="Tetraodon nigroviridis"

/mol\_type="genomic DNA"

/db\_xref="taxon:99883"

/clone="021G13"

/clone\_lib="S"

/note="Genoscope sequence ID : C0BG021AD07LP1-end : T7"

ORIGIN

Query Match Score 38.8; DB 9; Length 963;

Best Local Similarity 69.3%; Pred. No. 44; Matches 52; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

RESULT 11 AZ522110/c LOCUS AZ522110 DEFINITION 202Pb04 pb MBN #21 Plasmid berghei genomic 3 , genomic survey

Qy 55 CAACATTAACAAACAAACAAACAAACATTATAACATTACATTAC 114

Db 298 CAACAAACAAACAAACAAACAAACAAACATTACATTACATTAT 239

Qy 115 ATCTAGATAAACAT 129

Db 238 AATMATAATAAT 224

RESULT 10 AA846861 LOCUS AA846861 DEFINITION 523 bp mRNA linear EST 04-MAR-1998 3' similar to contains Alu repetitive element; mRNA sequence.

ACCESSION AA846861.1

VERSION EST

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 523)

ACCESSION NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.

VERSION 1

KEYWORDS National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

SOURCE Tumor Gene Index

ORGANISM Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium URL at: www-bio.llnl.gov/bbcrp/image/image.html  
Seq primer: -40ml3 Fwd. ET: from Amersham  
High quality sequence stop: 446.

FEATURES Source

1. .523 /organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1392980"  
/sex="male"  
/lab\_host="DH10B"  
/clone\_lib="Soares testis NHT"  
/note="Vector: pT7-3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo(dT) primer [5'-TGTTACGATCTGAAGTGGAGCGGCCATTTTTTTTTTT 3' ]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7-3 vector. Library went through one round of normalization to Cor5, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match Score 38.2; DB 1; Length 523;

Best Local Similarity 59.8%; Pred. No. 61; Matches 64; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 21 ATTICATTTGGAATTGACGTGTGTGATTTCACAATTACAAAC 80

Db 237 AATTCATTTGCATTACAGCAGTTATATTGTAGGAATGAAACCACATGCAATA 296

Qy 81 CAAACAAACATTACAAATTACTATTACAAATTACATCTAGATAACA 127

Db 297 AAACCAAATGAAAAAAAATAGTAAATTTATTATTTACTCA 343

RESULT 11 AZ522110/c LOCUS AZ522110 DEFINITION 202Pb04 pb MBN #21 Plasmid berghei genomic 3 , genomic survey

ACCESSION AZ522110 VERSION AZ522110.1

KEYWORDS GSS.

ORGANISM Plasmid berghei

ORGANISM Plasmid berghei

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 530)

REFERENCE Carlton,J.M.-R. and Dame,J.B.

ACCESSION AA846861

VERSION 1

KEYWORDS The Plasmodium vivax and P. berghei gene sequence tag projects

SOURCE Parasitol. Today (Regul. Ed.) 16 (10), 409 (2000)

COMMENT Contact: Dame JB  
Dept. of Pathobiology, College of Veterinary Medicine  
University of Florida  
215 SW 23rd Avenue, Bldg 1017, Gainesville, FL 32611, USA  
Tel: 352 392 4700

FEATURES	Class: shorgun. Location/Qualifiers 1..530 /organism="Plasmodium berghei" /mol_type="genomic DNA" /str="ANKA clone 15cy1 (clone of the ANKA 8417 clone)" /db_xref="taxon:5321" /dev_state="asexual blood forms" /lab_host="Mus musculus" /clone_lib="db MBR #21" /note="Vector: pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP; Site 1: EcoRV; Site 2: EcoRV; Genomic DNA was prepared from asynchronous b1lood stage forms of the cloned ANKA isolate of <i>P. berghei</i> grown in laboratory Swiss white mice. The DNA was purified from contaminating host DNA by Hoechst Dye 33258-0sCl ultracentrifugation and digested with mung bean nuclease. Purified DNA was digested with formamide at 50 C, as described (Vernick, R.B., and McCutchan, T.P. 1988. Nucleic Acids Research 16: 6883-6896). The ends of the digestion fragments were polished using T4 DNA Polymerase, and the fragments size selected in the range 500-200 bp. These were ligated into the EcoRV-cleaved and dephosphorylated pBluescript SK(+) vector. Recombinant plasmids were used to transform E. coli XL1-Gold host cells."	ORIGIN		
Query Match	Score 37.8; DB 8; Length 530; Best Local Similarity 57.0%; Pred. No. 76; Matches 69; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	Qy 10 ATAGGAGTTCAATTGGATGGACACTGTCTCATTCACATTACACA 69 Db 530 ATTGAAGTTGTAGCTGAGTAGTAACTCTCTCATCCAAACATTATGTA 471 Qy 70 ACAACAAACAAACACATTATAACATTACTATTACATTACATTACATA 129 Db 470 TAATAAACCTATAAGGATAAGTACAAATTGTATATAAAATTTATA 411 Qy 130 G 130 Db 410 G 410	RESULT 12 CNS04LX9/c DEFINITION Tetraodon nigroviridis genome survey sequence 979 bp linear GSS 01-SEP-2000 AL296694.1 GSS; genome survey sequence.	CNS04LX9 DEFINITION Tetraodon nigroviridis genome survey sequence 979 bp linear GSS 01-SEP-2000 AL296694.1 GSS; genome survey sequence.
KEYWORDS	Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleosteii; Acanthomorpha; Acanthopercygii; Percormorpha; Tetraodontiformes; Tetradontidae; Tetraodontidae; Tetraodon.	KEYWORDS Tetraodon nigroviridis Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina; Poidae; Triticeae; Hordeum vulgare subsp. spontaneum		
SOURCE	Roest Crollius,H., Fizames,C., Saurin,W., and Weissenbach,J., Bernot,A., Brottier,P., Quetier,F.,	SOURCE Hordeum vulgare subsp. spontaneum Unpublished (2002) Contact: Tadao Shin-i Center for Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Fax: 81-559-81-6856 Email: tshini@genes.nig.ac.jp		
ORGANISM	Roest Crollius,H., Fizames,C., Saurin,W., and Weissenbach,J., Bernot,A., Brottier,P., Quetier,F.,	ORGANISM Hordeum vulgare subsp. spontaneum Unpublished (2002) Contact: Tadao Shin-i Center for Genetic Resource Information National Institute of Genetics 111 Yata, Mishima, Shizuoka 411-8540, Japan Fax: 81-559-81-6856 Email: tshini@genes.nig.ac.jp		
REFERENCE	Estimate of human gene number provided by genome-wide analysis Nat. Genet. 25 (2), 235-238 (2000)	REFERENCE Authors Title Journal Medline Pubmed Reference Source 1..572 /organism="Hordeum vulgare subsp. spontaneum"		



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